

WHAT IS CLAIMED IS:

1. An isolated or recombinant polypeptide selected from the group consisting of: SEQ ID NOs:70, 71, 72, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, and 127, wherein at pH 5.5, said polypeptide has a fumonisin detoxification activity or a fumonisin derivative detoxification activity that is at least 1.5-fold greater than any of the polypeptides selected from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO.

2. The polypeptide of claim 1, wherein said polypeptide has a fumonisin detoxification activity that is at least 1.5-fold greater than any of the polypeptides selected from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO.

3. The polypeptide of claim 2, wherein the fumonisin detoxification activity comprises a fumonisin deamination reaction.

4. The polypeptide of claim 2, wherein said polypeptide has a fumonisin detoxification activity that is at least 20-fold greater than any of the polypeptides selected from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO.

5. The polypeptide of claim 2, wherein said polypeptide is encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs:67, 68, 69, 84, 86, 86, 99, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, and 126.

6. The polypeptide of claim 2, wherein said polypeptide is a fumonisin amine oxidase.

7. The polypeptide of claim 2, said polypeptide comprising a characteristic selected from the group consisting of:

a) wherein the optimum pH of said fumonisin detoxification activity is lower for said polypeptide than for any of the polypeptides selected from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO; and

b) wherein the thermostability of said fumonisin detoxification activity is higher for said polypeptide than for any of the polypeptides selected from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO.

8. The polypeptide of claim 2, wherein said polypeptide has increased fumonisin detoxification activity upon secretion from a eukaryotic cell relative to any of the polypeptides selected from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO.

9. The polypeptide of claim 8, wherein said eukaryotic cell is a plant cell.

10. The polypeptide of claim 8, wherein said eukaryotic cell is a fungal cell.

11. The polypeptide of claim 2, wherein said polypeptide comprises a leader sequence that directs the secretion of the polypeptide from a plant cell.

12. The polypeptide of claim 11, wherein said polypeptide leader is selected from the group consisting of an apoplast targeting sequence and a peroxisomal targeting sequence.

13. The polypeptide of claim 2, wherein the fumonisin being detoxified is selected from the group consisting of: a fumonisin B1; a fumonisin B2; a fumonisin B3; a fumonisin B4; and a fumonisin C1.

14. The polypeptide of claim 2, said polypeptide comprising a characteristic selected from the group consisting of:

a) wherein at pH 5.5 the k_{cat} of the fumonisin detoxification reaction catalyzed by the polypeptide is higher than the k_{cat} of the fumonisin detoxification reaction catalyzed by any of the polypeptides selected from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO;

b) wherein at pH 5.5 the fumonisin K_M for the fumonisin detoxification reaction catalyzed by the polypeptide is lower than the fumonisin K_M for the fumonisin detoxification reaction catalyzed by any of the polypeptides selected from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO; and

c) wherein at pH 5.5 the fumonisin k_{cat}/K_M of the fumonisin detoxification reaction catalyzed by the polypeptide is higher than the fumonisin k_{cat}/K_M of the fumonisin

detoxification reaction catalyzed by any of the polypeptides selected from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO.

15. A non-native variant of the polypeptide of claim 2, wherein one or more amino acids of the encoded polypeptide have been mutated.

16. The polypeptide of claim 2, further comprising a polypeptide purification subsequence.

17. The polypeptide of claim 2, wherein the polypeptide comprises an altered glycosylation site.

18. A polypeptide which is specifically bound by a polyclonal antisera raised against one or more antigen, the antigen comprising at least one sequence selected from the group consisting of SEQ ID NOs:70, 71, 72, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, and 127, wherein the antisera is subtracted with one or more polypeptide selected from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO.

19. A polypeptide which comprises a unique subsequence in a polypeptide selected from the group consisting of: SEQ ID NOs:70, 71, 72, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, and 127, wherein the unique subsequence is unique as compared to a polypeptide selected from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO.

20. An isolated or recombinant nucleic acid comprising a polynucleotide sequence that encodes a polypeptide selected from the group consisting of: SEQ ID NOs:70, 71, 72, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, and 127, or a complementary polynucleotide sequence thereof, wherein at pH 5.5 said polypeptide has a fumonisin detoxification activity or a fumonisin derivative detoxification activity that is at least 1.5-fold greater than any of the polypeptides selected from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO.

21. The nucleic acid of claim 20, wherein said polypeptide has a fumonisin detoxification activity that is at least 1.5-fold greater than any of the polypeptides selected

from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO.

22. The nucleic acid of claim 21, wherein the fumonisin detoxification activity comprises a fumonisin deamination reaction.

23. The nucleic acid of claim 21, wherein said polypeptide has a fumonisin detoxification activity that is at least 20-fold greater than any of the polypeptides selected from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO.

24. The nucleic acid of claim 21, wherein said nucleic acid is selected from the group consisting of SEQ ID NOs:67, 68, 69, 84, 86, 86, 99, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, and 126.

25. An isolated or recombinant nucleic acid comprising a polynucleotide sequence that encodes a polypeptide that at pH 5.5 has a fumonisin detoxification activity or a fumonisin derivative detoxification activity that is at least 1.5-fold greater than a polypeptide selected from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO; wherein said polynucleotide sequence hybridizes under high stringency conditions to a polynucleotide sequence selected from the group consisting of:

a) a polynucleotide sequence selected from the group consisting of SEQ ID NOs:67, 68, 69, 84, 86, 86, 99, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, and 126;

b) a polynucleotide sequence encoding a polypeptide selected from the group consisting of SEQ ID NOs:70, 71, 72, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, and 127;

c) a polynucleotide sequence complementary to the polynucleotide of a) or b); and

d) a polynucleotide sequence comprising a fragment of a) or b), wherein the fragment encodes a polypeptide having at least one fumonisin detoxification activity or at least one fumonisin derivative detoxification activity.

26. An isolated or recombinant nucleic acid comprising a polynucleotide sequence selected from the group consisting of:

a) a polynucleotide sequence selected from the group consisting of SEQ ID NOs:67, 68, 69, 84, 86, 86, 99, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, and 126;

b) a polynucleotide sequence encoding a polypeptide selected from the group consisting of SEQ ID NOs:70, 71, 72, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, and 127;

c) a polynucleotide sequence complementary to the polynucleotide of a) or b);

d) a polynucleotide sequence which hybridizes under highly stringent conditions over substantially the entire length of a polynucleotide sequence of any one of a), b), or c); and,

e) a polynucleotide sequence comprising a fragment of any one of a), b), c) or d), wherein the fragment encodes a polypeptide having at least one fumonisin detoxification activity or at least one fumonisin-derivative detoxification activity.

27. The nucleic acid of claim 26, wherein said polynucleotide sequence hybridizes under highly stringent conditions over substantially the entire length of a polynucleotide selected from the group consisting of:

a) a polynucleotide sequence encoding a polypeptide selected from the group consisting of SEQ ID NOs:70, 71, 72, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, and 127; and

b) a polynucleotide sequence complementary to the polynucleotide of a).

28. The nucleic acid of claim 26, wherein said polynucleotide sequence is selected from the group consisting of:

a) a polynucleotide sequence which hybridizes under highly stringent conditions over substantially the entire length of a polynucleotide sequence selected from the group consisting of SEQ ID NOs:67, 68, 69, 84, 86, 86, 99, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, and 126;

b) a polynucleotide sequence comprising a fragment of (a), wherein the fragment encodes a polypeptide having at least one fumonisin detoxification activity or at least one fumonisin-derivative detoxification activity; and

c) a polynucleotide sequence complementary to the polynucleotide of a) or b).

29. The nucleic acid of claim 28, wherein said polynucleotide sequence hybridizes under highly stringent conditions over substantially the entire length of a polynucleotide sequence selected from the group consisting of:

a) a polynucleotide sequence set forth in the group consisting of SEQ ID NOs:67, 68, 69, 84, 86, 86, 99, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, and 126; and

b) a polynucleotide complementary to the polynucleotide of a).

30. The nucleic acid of claim 21, wherein the polynucleotide encodes a fumonisins amine oxidase.

31. The nucleic acid of claim 21, wherein said nucleic acid comprises a characteristic selected from the group consisting of:

a) wherein the optimum pH of said fumonisins detoxification activity is lower for said polypeptide than for any of the polypeptides selected from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO; and

b) wherein the thermostability of said fumonisins detoxification activity is higher for said polypeptide than for any of the polypeptides selected from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO.

32. The nucleic acid of claim 21, wherein said polypeptide has increased fumonisins detoxification activity upon secretion from a eukaryotic cell relative to any of the polypeptides selected from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO.

33. The nucleic acid of claim 32, wherein said eukaryotic cell is a plant cell.

34. The nucleic acid of claim 32, wherein said eukaryotic cell is a fungal cell.

35. The nucleic acid of claim 21, wherein said polypeptide comprises a leader sequence that directs the secretion of the polypeptide from a plant cell.

36. The nucleic acid of claim 21, wherein said polypeptide leader sequence is selected from the group consisting of an apoplast targeting sequence and a peroxisomal targeting sequence.

37. The nucleic acid of claim 21, wherein the fumonisin is selected from the group consisting of: a fumonisin B1; a fumonisin B2; a fumonisin B3; a fumonisin B4; and a fumonisin C1.

38. The nucleic acid of claim 21, wherein said nucleic acid comprises a characteristic selected from the group consisting of:

a) wherein at pH 5.5, the k_{cat} of the fumonisin detoxification reaction catalyzed by the polypeptide is higher than the k_{cat} of the fumonisin detoxification reaction catalyzed by any of the polypeptides selected from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO;

b) wherein at pH 5.5, the fumonisin K_M for the fumonisin detoxification reaction catalyzed by the polypeptide is lower than the fumonisin K_M for the fumonisin detoxification reaction catalyzed by the polypeptides selected from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO; and

c) wherein at pH 5.5, the fumonisin k_{cat}/K_M of the fumonisin detoxification reaction catalyzed by the polypeptide is higher than the fumonisin k_{cat}/K_M of the fumonisin detoxification reaction catalyzed by any of the polypeptides selected from the group consisting of: SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; and any wild-type APAO.

39. The nucleic acid of claim 21, comprising a promoter operably linked to the polynucleotide.

40. The nucleic acid of claim 39, wherein the promoter is tissue-specific.

41. A non-native variant of the nucleic acid of claim 21, wherein one or more amino acids of the encoded polypeptide have been mutated.

42. A nucleic acid construct comprising a promoter operably linked to the polynucleotide of claim 21.

43. The nucleic acid construct of claim 42, wherein the promoter is heterologous with respect to the polynucleotide and effective to cause sufficient expression of the encoded polypeptide to cause the detoxification of fumonisin.

44. The nucleic acid construct of claim 43, wherein the polynucleotide sequence of claim 21 functions as a selectable marker.

45. The nucleic acid construct of claim 43, wherein a parental codon of the polynucleotide sequence of claim 21 has been replaced by a synonymous codon that is preferentially used in a plant relative to the parental codon.

46. The nucleic acid construct of claim 42, wherein the construct is a vector.

47. The vector of claim 46, wherein the vector comprises a first polynucleotide sequence comprising the promoter operably linked to the polynucleotide of claim 22 and a second polynucleotide sequence encoding a second polypeptide that confers a detectable phenotypic trait upon a cell or organism expressing the second polypeptide at an effective level.

48. The vector of claim 47, wherein the detectable phenotypic trait consists of one or more traits selected from the group consisting of: herbicide resistance; pest resistance; and a visible marker.

49. The vector of claim 46 wherein the vector comprises a T-DNA sequence.

50. The vector of claim 46, wherein the vector is a plant transformation vector.

51. A cell comprising at least one nucleic acid of claim 21, wherein the nucleic acid is heterologous to the cell.

52. The cell of claim 51, wherein the polynucleotide of claim 21, is operably linked to a regulatory sequence.

53. A cell transduced by the vector of claim 47.

54. The cell of claim 51, wherein the cell is a transgenic plant cell.

55. The transgenic plant cell of claim 54, wherein the plant cell expresses an exogenous polypeptide with fumonisin detoxification activity.

56. The cell of claim 55, wherein the fumonisin is a class B fumonisin.

57. The cell of claim 55, wherein the fumonisin is FB1.
58. A transgenic organism comprising the nucleic acid of claim 21 or the cell of claim 53.
59. The transgenic organism of claim 58, wherein the organism is a plant.
60. The transgenic plant of claim 59, wherein the plant is selected from the group of genera consisting of: *Fragaria*, *Lotus*, *Medicago*, *Onobrychis*, *Trifolium*, *Trigonella*, *Vigna*, *Citrus*, *Linum*, *Geranium*, *Manihot*, *Daucus*, *Arabidopsis*, *Brassica*, *Raphanus*, *Sinapis*, *Atropa*, *Capsicum*, *Datura*, *Hyoscyamus*, *Lycopersicon*, *Nicotiana*, *Solanum*, *Petunia*, *Digitalis*, *Majorana*, *Cichorium*, *Helianthus*, *Lactuca*, *Bromus*, *Asparagus*, *Antirrhinum*, *Heterocallis*, *Nemesia*, *Pelargonium*, *Panicum*, *Pennisetum*, *Ranunculus*, *Senecio*, *Salpiglossis*, *Cucumis*, *Browaalia*, *Lolium*, *Malus*, *Apium*, *Gossypium*, *Vicia*, *Lathyrus*, *Lupinus*, *Pachyrhizus*, *Wisteria*, and *Stizolobium*.
61. The transgenic plant of claim 59, wherein the plant is a crop plant selected from the group of genera consisting of: *Agrostis*, *Phleum*, *Dactylis*, *Sorgum*, *Setaria*, *Zea*, *Oryza*, *Triticum*, *Secale*, *Avena*, *Hordeum*, *Saccharum*, *Poa*, *Festuca*, *Stenotaphrum*, *Cynodon*, *Coix*, *Olyraeae*, *Phareae*, *Glycine*, *Pisum*, *Cicer*, *Phaseolus*, *Lens*, and *Arachis*.
62. The transgenic plant of claim 59, wherein the plant is selected from the group consisting of: corn, rice, cotton, soybean, sorghum, wheat, oat, barley, millet, sunflower, rapeseed, canola, pea, bean, lentil, peanut, yam, bean, cowpea, velvet bean, clover, alfalfa, lupine, vetch, lotus, sweet clover, wisteria, sweetpea, and a nut plant.
63. The transgenic plant of claim 62, wherein the plant is corn.
64. A seed produced by the transgenic plant of claim 62.
65. The transgenic organism of claim 58, wherein the organism is a microorganism.
66. A composition comprising at least two different nucleic acids of claim 21.
67. The composition of claim 66 comprising at least ten different nucleic acids of claim 21.
68. A composition produced by cleaving one or more nucleic acids of claim 21.
69. A nucleic acid which comprises a unique subsequence in a nucleic acid selected from the group consisting of SEQ ID NOs:67, 68, 69, 84, 86, 86, 99, 92, 94, 96, 98, 100, 102,

104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, and 126, wherein the unique subsequence is unique as compared to a nucleic acid selected from the group consisting of: SEQ ID NO:53; SEQ ID NO:55; SEQ ID NO:57; SEQ ID NO:59; SEQ ID NO:61; SEQ ID NO:63; and any wild-type APAO.

70. A method of detoxifying, degrading, neutralizing, or modifying at least one mycotoxin or mycotoxin-derivative, comprising incubating the at least one mycotoxin or mycotoxin-derivative and at least one polypeptide of claim 2, wherein the at least one polypeptide detoxifies, degrades, neutralizes or modifies the at least one mycotoxin or mycotoxin-derivative.

71. The method of claim 70, wherein the mycotoxin or mycotoxin derivative is selected from the group consisting of: a fumonisin; a fumonisin derivative; and a fumonisin analog.

72. The method of claim 71, wherein the fumonisin, fumonisin derivative or fumonisin analog is present in harvested grain.

73. The method of 71, wherein detoxification, degradation, neutralization or modification occurs during the processing of harvested grain.

74. A method of producing a polypeptide, the method comprising:

- a) introducing into a population of cells a nucleic acid of claim 21, the nucleic acid operatively linked to a regulatory sequence effective to produce the encoded polypeptide;
- b) culturing the cells in a culture medium to produce the polypeptide; and,
- c) isolating the polypeptide from the cells or from the culture medium.

75. A method of producing a transgenic plant or plant cell comprising:

- a) transforming a plant or plant cell with a polynucleotide of claim 21; and
- b) optionally regenerating a transgenic plant from the transformed plant cell.

76. A method for selecting a plant or cell containing a nucleic acid construct, the method comprising:

- a) providing a transgenic plant or cell containing a nucleic acid construct, wherein the nucleic acid construct comprises a nucleic acid of claim 21; and

- b) growing the plant or cell in the presence of a fumonisin under conditions where a polypeptide is expressed at an effective level, whereby the transgenic plant or cell grows at a

rate that is discernibly greater than the plant or cell would grow if it did not contain the nucleic acid construct.

77. A method of reducing pathogenicity of a fungus producing fumonisin comprising:

a) providing a transgenic cell containing the nucleic acid of claim 21 operably linked to a promoter, wherein the nucleic acid is heterologous to the cell; and

b) expressing the nucleic acid at a level effective to detoxify fumonisin, thereby reducing the pathogenicity of the fungus.

78. The method of claim 77, wherein the cell is selected from the group consisting of:

a) a plant cell residing in a plant;

b) a microorganism; and

c) a cell comprising a fumonisin esterase encoding polynucleotide operably linked to a promoter.

79. A method of detecting fumonisins comprising:

a) introducing the polypeptide of claim 2, into a sample containing fumonisin;

b) allowing the polypeptide to catalyze the deamination of fumonisin; and,

c) detecting a product of the deamination reaction.

80. The method of claim 79, wherein the product of the deamination reaction that is detected is ammonia or hydrogen peroxide.

81. A transgenic plant or transgenic plant explant that expresses the polypeptide of claim 2.

82. The transgenic plant or transgenic plant explant of claim 81 that further expresses a polypeptide selected from the group consisting of: a polypeptide having fumonisin modification activity; a polypeptide having chitinase activity; a polypeptide having antifungal activity; a polypeptide having mycotoxin detoxification activity; a polypeptide having

herbicidal activity; a polypeptide having pesticidal activity; and a polypeptide having nematocidal activity.

83. The transgenic plant or transgenic plant explant of claim 82 that expresses fumonisin esterase activity.

84. The transgenic plant or transgenic plant explant of claim 82 wherein the further expressed polypeptide functions as a selectable marker.

85. The transgenic plant or transgenic plant explant of claim 84, wherein the selectable marker consists of one or more markers selected from the group consisting of herbicide resistance, pest resistance, and visible markers.

86. A method of reducing pathogenicity of a fungus producing fumonisin comprising:

- a) providing a transgenic cell containing the nucleic acid of claim 21, operably linked to a promoter, wherein the nucleic acid is heterologous to the cell; and,
- b) expressing the nucleic acid at a level effective to produce sufficient H_2O_2 to reduce fungal infection.

87. The method of claim 86, wherein the cell is a plant cell residing in a plant.

88. The method of claim 86, wherein the cell comprises a fumonisin esterase encoding polynucleotide operably linked to a promoter.

89. A method of producing a transgenic organism, the method comprising:

- a) introducing into an organism, a nucleic acid of claim 21; and,
- b) expressing a polypeptide encoded by the nucleic acid at a level effective to deaminate fumonisin.

90. The method of claim 89, wherein the organism is selected from the group consisting of: a plant; a fungus; and a bacteria.

91. A method for creating or enhancing disease resistance in a plant, said method comprising:

- a) introducing into a plant cell a recombinant expression cassette comprising the nucleic acid of claim 21, operably linked to a promoter that drives expression in a plant, wherein said nucleic acid is selected from the group consisting of:

i) a nucleic acid encoding a polypeptide, wherein said polypeptide is selected from the group consisting of SEQ ID NOs:70, 71, 72, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, and 127; and

ii) a nucleic acid selected from the group consisting of SEQ ID NOs:67, 68, 69, 84, 86, 86, 99, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, and 126;

b) culturing the plant cell under plant cell growing conditions; and

c) regenerating from the plant cell a whole plant, wherein the plant has enhanced or newly created disease resistance.

92. The transgenic plant of claim 91, wherein the plant is selected from the group of genera consisting of: *Fragaria*, *Lotus*, *Medicago*, *Onobrychis*, *Trifolium*, *Trigonella*, *Vigna*, *Citrus*, *Linum*, *Geranium*, *Manihot*, *Daucus*, *Arabidopsis*, *Brassica*, *Raphanus*, *Sinapis*, *Atropa*, *Capsicum*, *Datura*, *Hyoscyamus*, *Lycopersicon*, *Nicotiana*, *Solanum*, *Petunia*, *Digitalis*, *Majorana*, *Cichorium*, *Helianthus*, *Lactuca*, *Bromus*, *Asparagus*, *Antirrhinum*, *Heterocallis*, *Nemesia*, *Pelargonium*, *Panicum*, *Pennisetum*, *Ranunculus*, *Senecio*, *Salpiglossis*, *Cucumis*, *Browaalia*, *Lolium*, *Malus*, *Apium*, *Gossypium*, *Vicia*, *Lathyrus*, *Lupinus*, *Pachyrhizus*, *Wisteria*, and *Stizolobium*.

93. The transgenic plant of claim 91, wherein the plant is a crop plant selected from the group of genera consisting of: *Agrostis*, *Phleum*, *Dactylis*, *Sorgum*, *Setaria*, *Zea*, *Oryza*, *Triticum*, *Secale*, *Avena*, *Hordeum*, *Saccharum*, *Poa*, *Festuca*, *Stenotaphrum*, *Cynodon*, *Coix*, *Olyrae*, *Phareae*, *Glycine*, *Pisum*, *Cicer*, *Phaseolus*, *Lens*, and *Arachis*.

94. The transgenic plant of claim 91, wherein the plant is selected from the group consisting of: corn, rice, cotton, soybean, sorghum, wheat, oat, barley, millet, sunflower, rapeseed, canola, pea, bean, lentil, peanut, yam, bean, cowpea, velvet bean, clover, alfalfa, lupine, vetch, lotus, sweet clover, wisteria, sweetpea, and a nut plant.

95. The transgenic plant of claim 94, wherein the plant is corn.

96. A seed produced by the transgenic plant of claim 94.